```
=> file reg; d que l3
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STRUCTURE FILE UPDATES:   23 APR 2001  HIGHEST RN 332094-77-6
DICTIONARY FILE UPDATES:  23 APR 2001  HIGHEST RN 332094-77-6

TSCA INFORMATION NOW CURRENT THROUGH January 11, 2001

  Please note that search-term pricing does apply when
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Structure search limits have been increased.  See HELP SLIMIT
for details.

L2          4853 SEA FILE=REGISTRY ABB=ON  PLU=ON  GGAAGTAAAAGTCGTAACAAGG|CCTTGT
                 TACGACTTTTACTTCC|GTATCCCTACCTGATCCGAGG|CCTCGGATCAGGTAGGGATAC/SQ
                 SN
L3             4 SEA FILE=REGISTRY ABB=ON  PLU=ON  L2 AND SQL<50

=> d rn cn kwic l3 1-4

L3   ANSWER 1 OF 4  REGISTRY  COPYRIGHT 2001 ACS
RN   259362-62-4  REGISTRY
CN   GenBank AR069841 (9CI)  (CA INDEX NAME)
SQL  24

SEQ      1 gaggaagtaa aagtcgtaac aagg
           ======== ========== ====

HITS AT:   3-24

L3   ANSWER 2 OF 4  REGISTRY  COPYRIGHT 2001 ACS
RN   222650-53-5  REGISTRY
CN   GenBank AR017906 (9CI)  (CA INDEX NAME)
SQL  22

SEQ      1 ggaagtaaaa gtcgtaacaa gg
           ========== ========== ==

HITS AT:   1-22

L3   ANSWER 3 OF 4  REGISTRY  COPYRIGHT 2001 ACS
RN   160872-92-4  REGISTRY
CN   DNA, d(G-G-A-A-G-T-A-A-A-A-G-T-C-G-T-A-A-C-A-A-G-G) (9CI)  (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN   Deoxyribonucleic acid, d(G-G-A-A-G-T-A-A-A-A-G-T-C-G-T-A-A-C-A-A-G-G)
OTHER NAMES:
CN   50: PN: WO0073499 SEQID: 44 claimed DNA
CN   54: PN: WO0073499 SEQID: 46 claimed DNA
CN   Deoxyribonucleic acid (primer ITS5 for 5.8 S ribosomal RNA gene-internal
     transcribed spacer region of root-infecting fungi)
CN   PN: WO9946405 SEQID: 99 unclaimed sequence
CN   PN: WO9947927 SEQID: 3 unclaimed DNA
SQL  22

SEQ      1 ggaagtaaaa gtcgtaacaa gg
           ========== ========== ==

HITS AT:   1-22
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Seq 1-2 and their complements

Sequence length less than 50.

L7 SQL = sequence length

Use registry number to match sequence to citation

L3 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2001 ACS
RN 147175-43-7 REGISTRY
CN DNA, d(C-C-C-G-G-A-A-T-T-C-G-G-A-A-G-T-A-A-A-A-G-T-C-G-T-A-A-C-A-A-G-G) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(C-C-C-G-G-A-A-T-T-C-G-G-A-A-G-T-A-A-A-A-G-T-C-G-T-A-A-C-A-A-G-G)
SQL **32**

SEQ 1 cccggaattc ggaagtaaaa gtcgtaacaa gg
========== ========== ==
HITS AT: 11-32

=> file caplus
FILE 'CAPLUS' ENTERED AT 10:33:04 ON 24 APR 2001
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FILE COVERS 1947 - 24 Apr 2001 VOL 134 ISS 18
FILE LAST UPDATED: 23 Apr 2001 (20010423/ED)

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=> d que l4
L2 4853 SEA FILE=REGISTRY ABB=ON PLU=ON GGAAGTAAAAGTCGTAACAAGG|CCTTGT TACGACTTTTACTTCC|GTATCCCTACCTGATCCGAGG|CCTCGGATCAGGTAGGGATAC/SQ SN
L3 4 SEA FILE=REGISTRY ABB=ON PLU=ON L2 AND SQL<50
L4 17 SEA FILE=CAPLUS ABB=ON PLU=ON L3

=> d ibib ab hitrn l4 1-17

L4 ANSWER 1 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:861843 CAPLUS
DOCUMENT NUMBER: 134:26058
TITLE: Nucleic acid probes, PCR primers and methods for detecting and identifying clinically important fungal pathogens
INVENTOR(S): Smith, Terry; Maher, Majella; Martin, Cara; Jannes, Geert; Rossau, Rudi; Van der Weide, Marjo
PATENT ASSIGNEE(S): Innogenetics N.V., Belg.; Enterprise Ireland (Trading as Bioresearch Ireland)
SOURCE: PCT Int. Appl., 59 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000073499	A2	20001207	WO 2000-EP4714	20000524

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: EP 1999-870109 A 19990528
US 1999-138621 P 19990611

AB The current invention relates to the field of detection and identification of clin. important fungi. More particularly, the present invention relates to species specific probes and PCR primers originating from the internal transcribed spacer (ITS) region of rDNA for the detection of fungal species such as Candida albicans, Candida parapsilosis, Candida tropicalis, Candida kefyr, Candida krusei, Candida glabrata, Candida dubliniensis, Aspergillus flavus, Aspergillus versicolor, Aspergillus nidulans, Aspergillus fumigatus, Cryptococcus neoformans and Pneumocystis carinii in clin. samples, and methods using said probes and PCR primers.
IT **160872-92-4P**
RL: ARG (Analytical reagent use); PRP (Properties); SPN (Synthetic preparation); ANST (Analytical study); PREP (Preparation); USES (Uses)
(nucleic acid primer sequence; nucleic acid probes, PCR primers and methods for detecting and identifying clin. important fungal pathogens)

L4 ANSWER 2 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:659157 CAPLUS
DOCUMENT NUMBER: 134:158182
TITLE: Genetic similarity among Cercospora apii-group species and their detection in host plant tissue by PCR/RFLP analyses of the rDNA internal transcribed spacer (ITS)
AUTHOR(S): Siboe, George M.; Murray, Johanne; Kirk, Paul M.
CORPORATE SOURCE: Department of Botany, University of Nairobi, Nairobi, Kenya
SOURCE: J. Gen. Appl. Microbiol. (2000), 46(2), 69-78
CODEN: JGAMA9; ISSN: 0022-1260
PUBLISHER: Microbiology Research Foundation
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The objective of this study was to det. the genetic relatedness among the

Cercospora and Pseudocercospora species closely related to Cercospora apii by using a polymerase chain reaction/restriction fragment length polymorphism (PCR/RFLP) anal. of the internal transcribed spacer (ITS) region. A single PCR fragment (about 550 bp) was obtained from all Cercospora species categorized as the C. apii-group, Pseudocercospora purpurea, Pseudocercospora conyzae, and Pseudocercospora cavarae. Cercospora caricis yielded a 680 bp PCR fragment. The similarity in the PCR fragment size and RFLP profiles among the C. apii-group isolates, including Pseudocercospora purpurea, and Pseudocercospora conyzae strongly suggests that these species are conspecific. Synonymy with C. apii (lectotype) at a subspecific rank has been proposed. Amplified ITS regions of genomic DNA extd. from spinach leaves showing 12 and 23% leaf spot disease symptoms caused by Cercospora beticola yielded two PCR fragments (i.e., one from the fungus and one from the host plant) and were resolved by electrophoresis of the PCR product in 3% LMP agarose. Digestion of the total PCR product with HinfI restriction enzyme yielded RFLP profiles similar to those obtained from amplified DNA from the causative agent, C. beticola. The method described in this preliminary study offers rapid detection and diagnosis of fungal infections in plants for disease prediction and management and screening of plant materials for quarantine purposes.

IT **160872-92-4**, DNA, d(G-G-A-A-G-T-A-A-A-A-G-T-C-G-T-A-A-C-A-A-G-G)
RL: AGR (Agricultural use); ARG (Analytical reagent use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(genetic similarity among Cercospora apii-group species and their detection in host plant tissue by PCR/RFLP analyses of rDNA internal transcribed spacer (ITS))

REFERENCE COUNT: 45
REFERENCE(S):
(2) Bridge, P; Applications of PCR in Mycology 1998, P63 CAPLUS
(3) Buscot, F; Mycol Res 1996, V100, P63 CAPLUS
(4) Chen, W; Exp Mycol 1992, V16, P22 CAPLUS
(5) Chillali, M; J Gen Appl Microbiol 1997, V43, P23 CAPLUS
(12) Dover, G; Nature 1982, V299, P111 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 3 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:214300 CAPLUS
DOCUMENT NUMBER: 133:172656
TITLE: PCR detection of Fusarium oxysporum f.sp. gladioli race 1, causal agent of Gladiolus yellows disease, from infected corms
AUTHOR(S): De Haan, L. A. M.; Numansen, A.; Roebroeck, E. J. A.; Van Doorn, J.
CORPORATE SOURCE: Bulb Research Centre, Lisse, 2160 AB, Neth.
SOURCE: Plant Pathol. (2000), 49(1), 89-100
CODEN: PLPAAD; ISSN: 0032-0862
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Fusarium oxysporum f.sp. gladioli (FOG) race 1 infects both large- and small-flowered Gladiolus cultivars. Race 2 isolates infect only small-flowered cultivars but can be present as epiphytes on large-flowered plants. When 160 arbitrary 10-mer oligonucleotide primers were tested on FOG by PCR to find RAPD markers specific for race 1, the RAPD primer G12 amplified two discriminating DNA fragments, AB (609 bp) and EF (1196 bp), in race 1 isolates only. Both fragments were cloned and sequenced. Two pairs of race 1-specific primers for multiplex PCR were designed. Tests of 112 F. oxysporum isolates by PCR showed that, in almost all cases, race 1 isolates of vegetative compatibility group 0340 could be distinguished

with these primers. Seven putative race 1 isolates did not react in multiplex PCR; hybridization studies with labeled AB and EF DNA fragments showed that these isolates belong to sep. groups. A bioassay was developed to detect corms that were latently infected with FOG race 1. Gladiolus corms were homogenized and incubated for 5 days at 28.degree.C in a semiselective medium to induce growth of Fusarium. Cultivated mycelium was isolated and subjected to the developed multiplex PCR after std. DNA isolation or disruption by microwave treatment.

IT **160872-92-4**
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence of useful primer; PCR detection of Fusarium oxysporum f.sp. gladioli race 1, causal agent of Gladiolus yellows disease, from infected corms)

REFERENCE COUNT: 38
REFERENCE(S):
(2) Assigbetse, K; Phytopathology 1994, V84, P622 CAPLUS
(4) Bates, M; Journal of Biological Chemistry 1993, V268, P14757 CAPLUS
(7) Crowhurst, R; Current Genetics 1991, V20, P391 CAPLUS
(8) De Boer, S; Nucleic Acids Research 1995, V23, P2567 CAPLUS
(10) Ellsworth, D; Biofeedback 1993, V14, P214 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 4 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:83961 CAPLUS
DOCUMENT NUMBER: 132:246893
TITLE: Genetic identification of Candida species in HIV-positive patients using the polymerase chain reaction and restriction fragment length polymorphism analysis of its DNA
AUTHOR(S): Irobi, J.; Schoofs, A.; Goossens, H.
CORPORATE SOURCE: Department of Biochemistry, University of Antwerp, UIA, Antwerp, Belg.
SOURCE: Mol. Cell. Probes (1999), 13(6), 401-406
CODEN: MCPRE6; ISSN: 0890-8508
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The polymerase chain reaction was used to amplify a targeted region: an internal transcribed spacer region of the ribosomal DNA from 114 Candida isolates and 65 ref. strains. Unique product sizes were obtained for Candida glabrata, C. guillermondii and C. inconspicua. Isolates of C. albicans, C. tropicalis, C. dubliniensis and C. krusei could be identified following restriction digestion of the PCR products. The methods proved to be both simple and reproducible and may offer potential advantages over phenotyping methods. (c) 1999 Academic Press.

IT **160872-92-4**, Deoxyribonucleic acid (primer ITS5 for 5.8 S ribosomal RNA gene-internal transcribed spacer region of root-infecting fungi)
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(genetic identification of Candida species in HIV-pos. patients using PCR and RFLP anal. of its DNA)

REFERENCE COUNT: 20
REFERENCE(S):
(2) Burgener-Kairuz, P; Journal of Clinical Microbiology 1994, V32, P1902 CAPLUS
(3) Fujita, S; Journal of Clinical Microbiology 1995,

V33, P962 CAPLUS
(4) Holmes, A; Journal of Clinical Microbiology 1994, V32, P228 CAPLUS
(6) Magee, B; Journal of Bacteriology 1987, V169, P1639 CAPLUS
(8) Molina, F; FEMS Microbiology Letters 1993, V108, P259 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 5 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:791900 CAPLUS
DOCUMENT NUMBER: 132:88869
TITLE: New PCR method to differentiate species in the Aspergillus niger aggregate
AUTHOR(S): Accensi, F.; Cano, J.; Figuera, L.; Abarca, M. L.; Cabanes, F. J.
CORPORATE SOURCE: Departament de Patologia i Produccio Animals (Microbiologia), Facultat de Veterinaria, Departament de Patologia i Produccio Animals (Microbiologia), Facultat de Veterinaria, Universitat Autonoma de Barcelona, Barcelona, 08193, Spain
SOURCE: FEMS Microbiol. Lett. (1999), 180(2), 191-196
CODEN: FMLED7; ISSN: 0378-1097
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The DNA that encodes the 5.8S gene of the rRNA and the two intergenic spacers ITS1 and ITS2 of the two proposed type strains of the Aspergillus niger aggregate (A. niger and Aspergillus tubingensis) have been sequenced. By comparison of sequences we have found that both species could be differentiated by RsaI digestion of the PCR products of the mentioned regions. This method could be a useful tool in the identification of strains of the A. niger aggregate, esp. in studies that involve a large no. of isolates.
IT **160872-92-4**
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR primer; 5.8S rRNA gene and intergenic spacer sequences in PCR method to differentiate species in Aspergillus niger aggregate)
REFERENCE COUNT: 20
REFERENCE(S): (1) Abarca, M; Appl Environ Microbiol 1994, V60, P2650 CAPLUS
(5) Gene, J; Antonie van Leeuwenhoek Int J Gen Mol Microbiol 1996, V70, P49 CAPLUS
(7) Kusters van Someren, M; Curr Genet 1991, V19, P21 CAPLUS
(11) Parenicova, L; Mycol Res 1997, V101, P810 CAPLUS
(14) Teren, J; Mycopathologia 1996, V134, P171 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 6 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:614256 CAPLUS
DOCUMENT NUMBER: 131:225830
TITLE: An equine Neospora isolate and its uses
INVENTOR(S): Marsh, Antoinette E.; Conrad, Patricia A.; Barr, Bradd C.
PATENT ASSIGNEE(S): The Regents of the University of California, USA
SOURCE: PCT Int. Appl., 48 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English

Searched by Barb O'Bryen & Toby Port

FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9947927	A1	19990923	WO 1999-US5754	19990316
W: AU, CA, JP				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6071737	A	20000606	US 1998-42600	19980316
AU 9931874	A1	19991011	AU 1999-31874	19990316
EP 1064550	A1	20010103	EP 1999-913906	19990316
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.: US 1998-42600 A 19980316
WO 1999-US5754 W 19990316

AB The present invention provides isolated equine Neospora cultures. The cultures are used to develop diagnostic assays for the detection of Neospora infection in horses and other animals. Also provided are pharmaceutical compns. for the treatment and prevention of Neospora infections.

IT **160872-92-4**
RL: PRP (Properties)
(unclaimed sequence; equine Neospora isolate and its uses)

REFERENCE COUNT: 2
REFERENCE(S): (1) Conrad; US 5707617 A 1998
(2) Conrad; US 5889166 A 1999 CAPLUS

L4 ANSWER 7 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:595415 CAPLUS
DOCUMENT NUMBER: 131:224450
TITLE: Detection of fermentation-related microorganisms by PCR of rDNA internal transcribed spacers
INVENTOR(S): Engel, Stacia R.; Descenzo, Richard A.; Morenzoni, Richard A.; Irelan, Nancy A.
PATENT ASSIGNEE(S): E. & J. Gallo Winery, USA
SOURCE: PCT Int. Appl., 53 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9946405	A1	19990916	WO 1999-US4251	19990311
W: AU, BR, CA, CN, JP, NZ				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9928810	A1	19990927	AU 1999-28810	19990311
EP 1062365	A1	20001227	EP 1999-909651	19990311
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.: US 1998-37990 A 19980311
WO 1999-US4251 W 19990311

AB Unique DNA sequences are provided which are useful in identifying different fermn.-related microorganisms, such as those involved in fermns. These unique DNA sequences can be used to provide oligonucleotide primers in PCR-based anal. for the identification of fermn.-related microorganisms. The DNA sequences of the present invention include the internal transcribed spacer (ITS) of the rRNA gene regions of particular

fermn.-related microorganisms, as well as oligonucleotide primers which are derived from these regions which are capable of identifying the particular microorganism.

IT **160872-92-4**
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(primer ITS5; detection of fermn.-related microorganisms by PCR of rDNA internal transcribed spacers)

REFERENCE COUNT: 2
REFERENCE(S): (1) Hamelin; US 5792611 A 1998 CAPLUS
(2) Lott; US 5631132 A 1997 CAPLUS

L4 ANSWER 8 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:507427 CAPLUS
DOCUMENT NUMBER: 131:332661
TITLE: Primers for genotyping single nucleotide polymorphisms and microsatellites in the pathogenic fungus Coccidioides immitis
AUTHOR(S): Fisher, Matthew C.; White, Thomas J.; Taylor, John W.
CORPORATE SOURCE: Department of Plant and Microbial Biology, University of California, Berkeley, CA, 94720, USA
SOURCE: Mol. Ecol. (1999), 8(6), 1082-1084
CODEN: MOECEO; ISSN: 0962-1083
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In this study, the authors describe the characterization and isolation of two classes of polymorphic genetic markers from the California species of Coccidioides immitis: (i) SNPs and (ii) microsatellites. Dure to their low mutation rates, SNP markers were isolated to test hypotheses about the mode of reprodn. in California Coccidioides immitis. The multi-allelic nature of microsatellites lends them to clinical diagnostic uses in both species of Coccidioides immitis simultaneously, and were isolated to this end. The authors are currently using these markers to generate data sets from panels of Coccidioides immitis that were isolated from clin. and environmental sources from a range of geog. locations spanning the entire distribution of this pathogen. Used together, these data will enable recent epidemiol. patterns to be characterized, as well as anal. of deeper evolutionary processes.

IT **160872-92-4**
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence of useful SNP primer; primers for genotyping single nucleotide polymorphisms and microsatellites in pathogenic fungus Coccidioides immitis)

REFERENCE COUNT: 7
REFERENCE(S): (1) Burt, A; Molecular Ecology 1994, V3, P523 CAPLUS
(3) Koufopanou, V; Proceedings of the National Academy of Sciences of the USA 1997, V94, P5478 CAPLUS
(4) Koufopanou, V; Proceedings of the National Academy of Sciences of the USA 1998, V95, P8414 CAPLUS
(6) Rassmann, K; Electrophoresis 1991, V12, P113 CAPLUS
(7) Zimmermann, C; Journal of Clinical Microbiology 1994, V32, P3040 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 9 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:390438 CAPLUS
DOCUMENT NUMBER: 131:42170
TITLE: Internal transcribed spacer sequences of grape

pathogenic fungi for detection of infection
INVENTOR(S): Engel, Stacia R.; Descenzo, Richard A.; Irelan, Nancy A.
PATENT ASSIGNEE(S): E. & J. Gallo Winery, USA
SOURCE: PCT Int. Appl., 43 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9929899	A1	19990617	WO 1998-US25210	19981207
W: AU, BR, CA, CN, JP, NZ				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6080543	A	20000627	US 1997-986727	19971208
ZA 9811183	A	19990609	ZA 1998-11183	19981207
AU 9916068	A1	19990628	AU 1999-16068	19981207
EP 1036196	A1	20000920	EP 1998-960484	19981207
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.: US 1997-986727 A 19971208
WO 1998-US25210 W 19981207

AB Internal transcribed spacers that can be used as markers to identify phytopathogenic fungi, esp. pathogens of grapes, are described. These unique DNA sequences can be used to provide oligonucleotide primers in PCR based anal. for the identification of fungal pathogens. Primers and probes for detection of these sequences are described.

IT **160872-92-4**
RL: AGR (Agricultural use); ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer for amplification rDNA of fungi in detection of grape pathogens; internal transcribed spacer sequences of grape pathogenic fungi for detection of infection)

REFERENCE COUNT: 2
REFERENCE(S):
(1) Peros; Phytopathology 1997, V87(8), P799
(2) Rehner; Canadian Journal of Botany 1994, V72, P1666 CAPLUS

L4 ANSWER 10 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:367864 CAPLUS
DOCUMENT NUMBER: 131:194967
TITLE: Identification of taxa in the genus Beta using ITS1 sequence information
AUTHOR(S): Shen, Yulong; Newbury, H. John; Ford-Lloyd, Brian V.
CORPORATE SOURCE: School of Biological Sciences, University of Birmingham, Birmingham, B15 2TT, UK
SOURCE: Plant Mol. Biol. Rep. (1998), 16(2), 147-155
CODEN: PMBRD4; ISSN: 0735-9640
PUBLISHER: Kluwer Academic Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Sequence variation in the ITS1 locus of the nuclear ribosomal DNA in beets has previously been used to reconstruct phylogeny of the species in the genus Beta. We have developed protocols that allow the identification of Beta taxa by use of taxon-specific primers. Beta sections, species and subspecies can be identified. Differences within the ITS1 region of a single base can be exploited for species identification. The results from

this study not only provide effective methods for wild beet identification, but also indicate the potential use of the techniques in other crops.

IT **160872-92-4**
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(primer ITS5; identification of taxa in genus Beta using ITS1 sequence information)

REFERENCE COUNT: 9
REFERENCE(S):
(1) Novy, R; Theor Appl Genet 1996, V92, P840 CAPLUS
(2) Reamon-Buttner, S; Genet Res Crop Evol 1996, V43, P261
(4) Sang, T; Proc Natl Acad Sci (USA) 1995, V92, P6813 CAPLUS
(6) Smith, R; Crop Sci 1994, V34, P1373 CAPLUS
(9) Wendel, J; Proc Natl Acad Sci (USA) 1995, V92, P280 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 11 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:212103 CAPLUS
DOCUMENT NUMBER: 131:68720
TITLE: A new pair of primers designed for amplification of the ITS region in Tuber species
AUTHOR(S): Bertini, Luana; Amicucci, Antonella; Agostini, Deborah; Polidori, Emanuela; Potenza, Lucia; Guidi, Chiara; Stocchi, Vilberto
CORPORATE SOURCE: Istituto di Chimica Biologica 'Giorgio Fornaini', Universita degli Studi di Urbino, Urbino, 61029, Italy
SOURCE: FEMS Microbiol. Lett. (1999), 173(1), 239-245
CODEN: FMLED7; ISSN: 0378-1097
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The alignment of the 28S gene of several species of Pezizales allowed selection of 2 pairs of primers able to amplify the internal transcribed spacer region of ribosomal DNA in mycorrhizal fungi, such as truffles. The higher yield of the amplification product demonstrates a better annealing of the new primers to the rDNA, as compared to the universal primers internal transcribed spacer 1 and internal transcribed spacer 4. Therefore, the new primers can be used as an easier and more sensitive tool for the identification of truffle species in any stage of their life cycle, including the mycorrhizal phase.

IT **160872-92-4**
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR primer ITS5; PCR primer pair designed for amplification of the ITS region in Tuber species)

REFERENCE COUNT: 13
REFERENCE(S):
(1) Amicucci, A; Biotechnol Lett 1996, V18, P821 CAPLUS
(2) Bertini, L; FEMS Microbiol Lett 1998, V164, P397 CAPLUS
(3) Gardes, M; Mol Ecol 1993, V2, P113 CAPLUS
(5) Henrion, B; Mycol Res 1994, V98, P37 CAPLUS
(6) Lanfranco, L; FEMS Microbiol Lett 1993, V114, P245 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 12 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:806388 CAPLUS

DOCUMENT NUMBER: 130:178018
TITLE: Identification of varieties by biochemical methods in Pleurotus spp.
AUTHOR(S): Kim, Dong-Hyun; Kong, Won-Sik; Kim, Kyung-Soo; Kim, Young-Ho; You, Chang-Hyun; Kim, Young-Bae
CORPORATE SOURCE: National Institute of Agricultural Science & Technology, RDA, Suwon, 441-707, S. Korea
SOURCE: Han'guk Kyunhakhoechi (1998), 26(2), 173-181
CODEN: HKCHDD; ISSN: 0253-651X
PUBLISHER: Korean Society of Mycology
DOCUMENT TYPE: Journal
LANGUAGE: Korean

AB To identify genetic difference of 13 strains in three Pleurotus species, analyses of rDNA, AP-PCR and RFLP were carried out. IGRI and ITSI-II regions of rDNA amplified by PCR were about 0.9 and 0.7 kb, resp. These PCR products were digested with six restriction enzymes to analyze polymorphism. Esp., treatment of HaeIII enzyme on ITSI-II regions showed specific bands in three Pleurotus sajor-caju strains. Genetic differences among three species were classified by similarity analyses based on rDNA polymorphism. Various band patterns of 2,500.apprx.150 bp were showed by AP-PCR. Identification of species and varieties in 13 Pleurotus strains was possible according to primers used in AP-PCR. In order to develop genetic markers, RFLPs using IGRI and ITSI.apprx.II probes derived from ASI 2180 and 2070 were carried out on eight Pleurotus varieties. RFLP patterns using IGRI probe were more various than that of ITSI.apprx.II probe.

IT **160872-92-4**
RL: ARU (Analytical role, unclassified); BPR (Biological process); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); PROC (Process); USES (Uses)
(primer; Pleurotus variety identification by biochem. methods)

L4 ANSWER 13 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:478983 CAPLUS
DOCUMENT NUMBER: 129:105218
TITLE: PCR assays for phytophthora species
INVENTOR(S): Ristaino, Jean B.
PATENT ASSIGNEE(S): North Carolina State University, USA
SOURCE: U.S., 12 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5780271	A	19980714	US 1996-748860	19961113

AB Methods of screening for the presence of specific Phytophthora species using oligonucleotide primers are discussed. Specific methods are presented to det. the presence of P. infestans in potato and tomato, and P. cactorum in tomato and other plant species. P. mirabilis can also be tested using the oligonucleotide probes. Thus, the test sample is lysed with Tris(hydroxymethyl) aminomethane buffer, to release possible fungal DNA, digested with HaeIII endonuclease, and subjected to PCR amplification. Typical test samples include mature plants and fruit from tomato, potato, strawberry, and apple. Diagnostic screening kits contg. the above mentioned reagents are also claimed.

IT **160872-92-4**
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)

(oligonucleotide primer; oligonucleotide primers and PCR assays for Phytophthora detection)

L4 ANSWER 14 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:540411 CAPLUS
DOCUMENT NUMBER: 125:213488
TITLE: PCR-based molecular discrimination of Verticillium chlamydosporium isolates
AUTHOR(S): Arora, D. K.; Hirsch, P. R.; Kerry, B. R.
CORPORATE SOURCE: Soil Science Department, IACR-Rothamsted, Harpenden, AL5 2JQ, UK
SOURCE: Mycol. Res. (1996), 100(7), 801-809
CODEN: MYCRER; ISSN: 0953-7562
DOCUMENT TYPE: Journal
LANGUAGE: English
AB PCR-based assays were performed to resolve the genetic variation between 28 different isolates of Verticillium chlamydosporium using primers designed to amplify ribosomal internal transcribed spacers (ITS) and intergenic spacers (IGS). Different isolates of V. chlamydosporium were also differentiated using primers matching enterobacterial repetitive intergenic consensus (ERIC) sequences and repetitive extragenic palindromic (REP) elements. Restriction fingerprinting of PCR-amplified ITS products failed to yield intraspecific polymorphism, and different levels of discrimination between V. chlamydosporium isolates were not achieved. However, restriction patterns of ITS products digested with HaeIII and HinfI were useful in differentiating between some of the closely related isolates of V. chlamydosporium, plant pathogenic Verticillium species, and some common soil fungi. PCR amplification of IGS was found to be the most sensitive method which enabled the detection of 22 variants within the sample of 28 isolates of V. chlamydosporium and 6 different plant pathogenic Verticillium species. By using ERIC and REP-PCR fingerprinting, isolates were categorized in 20 and 13 genotypes, resp. In general, PCR-based procedures can differentiate between closely related isolates of V. chlamydosporium within IGS genotypes. This also could be achieved by ERIC and REP-PCR, and may be considered a rapid tool for the genetic characterization and detection of different isolates of V. chlamydosporium.
IT **160872-92-4**
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer ITS5; PCR-based mol. discrimination of Verticillium chlamydosporium isolates)

L4 ANSWER 15 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:517462 CAPLUS
DOCUMENT NUMBER: 125:190152
TITLE: Polymerase chain reaction amplification and restriction analysis of the ribosomal DNA of Olpidium radicale isolates
AUTHOR(S): Jiang, Linghuo; Hiruki, Chuji
CORPORATE SOURCE: Department Agricultural, Food and Nutritional Science, University Alberta, Edmonton, AL, T6G 2P5, Can.
SOURCE: J. Microbiol. Methods (1996), 26(1,2), 87-93
CODEN: JMIMDQ; ISSN: 0167-7012
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A mol. method for discriminating Olpidium radicale cucurbit isolates is described, which combines amplification and restriction fragment length polymorphism (RFLP) anal. of a region including the ribosomal 5.8S gene and two internal transcribed spacers. Four single-sporangium isolates, representing the three host-specific strains of Olpidium radicale cucurbit group, were assayed by this method. Sizes of the region were found to be

approx. 1.3 kilobase (kb) in the three isolates except 1.9 kb in one isolate. Consistent RFLPs in this region were detected among the isolates of Olpidium radicale. The tobacco isolate of Olpidium brassicae did not produce any common band with the four isolates of Olpidium radicale after digestion with the three enzymes.

IT **160872-92-4**
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(primer for 5.8 S rRNA genes of Olpidium; PCR and restriction anal. of ribosomal DNA of Olpidium radicale isolates)

L4 ANSWER 16 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1995:9984 CAPLUS
DOCUMENT NUMBER: 122:124148
TITLE: Identification of fungi in the Gaeumannomyces-Phialophora complex by RFLPs of PCR-amplified ribosomal DNAs
AUTHOR(S): Ward, E.; Akrofi, A. Y.
CORPORATE SOURCE: Plant Pathol. Dep., AFRC Inst. Arable Crops Res., Harpenden/Herts, AL5 2JQ, UK
SOURCE: Mycol. Res. (1994), 98(2), 219-24
CODEN: MYCRER; ISSN: 0953-7562
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The polymerase chain reaction (PCR) was used to amplify ribosomal internal transcribed spacer and 5.8S DNA from isolates of Gaeumannomyces graminis, Phialophora graminicola, and other root-infecting fungi, isolated mostly from cereals and grasses. Different restriction enzymes were used to digest these amplified rDNAs to find polymorphisms useful in identification. Most of the enzymes tested were useful for discriminating between G. graminis and P. graminicola, and three enzymes (Dde I, Hae III and Hha I) could be used to distinguish between the varieties of G. graminis (tritici, avenae and graminis). However, a few atypical isolates gave intermediate RFLP patterns. The method was found to discriminate between Gaeumannomyces-Phialophora fungi and other organisms and to identify G. graminis var. tritici and P. graminicola on infected wheat roots. The approach is a useful addn. to the techniques available for the identification of fungi in the Gaeumannomyces-Phialophora complex.

IT **160872-92-4**
RL: PRP (Properties)
(PCR-RFLP of ribosomal DNAs method for identification of fungi in the Gaeumannomyces-Phialophora family)

L4 ANSWER 17 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1993:206087 CAPLUS
DOCUMENT NUMBER: 118:206087
TITLE: Strain typing in Lentinula edodes by polymerase chain reaction
AUTHOR(S): Kwan, Hoi Shan; Chiu, Siu Wai; Pang, Ka Ming; Cheng, Suk Chun
CORPORATE SOURCE: Dep. Biol., Chin. Univ. Hong Kong, Shatin, Hong Kong
SOURCE: Exp. Mycol. (1992), 16(2), 163-6
CODEN: EXMYD2; ISSN: 0147-5975
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Differences among strains of Lentinula edodes were examd. by the polymerase chain reaction using conserved rDNA-ITS sequences as specific primers (rDNA-PCR) and an M13 forward 24-mer sequencing primer as the arbitrary primer (AP-PCR). For rDNA-PCR, the ITS2 regions of three strains sequenced by the dideoxy chain-termination reaction revealed deletion/insertion and base substitution. For AP-PCR, almost every tested

strain had its unique DNA profile with some DNA bands common to all 15 strains tested. The complexity of the DNA profile does not correlate with the monokaryotic or dikaryotic nature of the strain. The cultivated dikaryotic strains showed heterogeneous genomic fingerprints. Also, polymorphic DNA markers were generated. Thus, AP-PCR can be conveniently applied for strain typing.

IT **147175-43-7**
RL: USES (Uses)
(as DNA primer for polymerase chain reaction, for strain typing of Lentinula edodes)

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